

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/592,918
Source: FWP
Date Processed by STIC: 9/25/06

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IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/592,918

DATE: 09/25/2006

TIME: 10:34:45

Input Set : A:\L7350.0011 SEQUENCE LISTING.txt
 Output Set: N:\CRF4\09252006\J592918.raw

3 <110> APPLICANT: Locomogene, Inc.
 5 <120> TITLE OF INVENTION: Pharmaceutical composition containing hsHRD3
 7 <130> FILE REFERENCE: L7350.0011
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/592,918
 C--> 9 <141> CURRENT FILING DATE: 2006-09-15
 9 <150> PRIOR APPLICATION NUMBER: JP 2004-76931
 10 <151> PRIOR FILING DATE: 2004-03-17
 12 <150> PRIOR APPLICATION NUMBER: JP 2004-314364
 13 <151> PRIOR FILING DATE: 2004-10-28
 15 <160> NUMBER OF SEQ ID NOS: 15
 17 <170> SOFTWARE: PatentIn version 3.2
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 7885
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (46)..(2427)
 29 <400> SEQUENCE: 1
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 31 Met Arg Val Arg
 32 1
 34 ata ggg ctg acg ctg ctg tgt gcg gtg ctg ctg agc ttg gcc tcg 105
 35 Ile Gly Leu Thr Leu Leu Cys Ala Val Leu Leu Ser Leu Ala Ser
 36 5 10 15 20
 38 gcg tcc tcg gat gaa gaa ggc agc cag gat gaa tcc tta gat tcc aag 153
 39 Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp Glu Ser Leu Asp Ser Lys
 40 25 30 35
 42 act act ttg aca tca gat gag tca gta aag gac cat act act gca ggc 201
 43 Thr Thr Leu Thr Ser Asp Glu Ser Val Lys Asp His Thr Thr Ala Gly
 44 40 45 50
 46 aga gta gtt gct ggt caa ata ttt ctt gat tca gaa gaa tct gaa tta 249
 47 Arg Val Val Ala Gly Gln Ile Phe Leu Asp Ser Glu Glu Ser Glu Leu
 48 55 60 65
 50 qaa tcc tct att caa gaa gag gaa gac agc ctc aag agc caa gag qgg 297
 51 Glu Ser Ser Ile Gln Glu Glu Asp Ser Leu Lys Ser Gln Glu Gly
 52 70 75 80
 54 gaa agt gtc aca gaa gat atc agc ttt cta gag tct cca aat cca gaa 345
 55 Glu Ser Val Thr Glu Asp Ile Ser Phe Leu Glu Ser Pro Asn Pro Glu
 56 85 90 95 100
 58 aac aag gac tat gaa gag cca aag aaa gta cggt aaa cca gct ttg acc 393
 59 Asn Lys Asp Tyr Glu Glu Pro Lys Lys Val Arg Lys Pro Ala Leu Thr
 60 105 110 115

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64	120 125 130	
66	ttc cta gat aag gag tat gat gaa tgt aca tca gat ggg agg gaa gat	489
67	Phe Leu Asp Lys Glu Tyr Asp Glu Cys Thr Ser Asp Gly Arg Glu Asp	
68	135 140 145	
70	ggc aga ctg tgg tgt gct aca acc tat gac tac aaa gca gat gaa aag	537
71	Gly Arg Leu Trp Cys Ala Thr Thr Tyr Asp Tyr Lys Ala Asp Glu Lys	
72	150 155 160	
74	tgg ggc ttt tgt gaa act gaa gaa gag gct gct aag aga cgg cag atg	585
75	Trp Gly Phe Cys Glu Thr Glu Glu Ala Ala Lys Arg Arg Gln Met	
76	165 170 175 180	
78	cag gaa gca gaa atg atg tat caa act gga atg aaa atc ctt aat gga	633
79	Gln Glu Ala Glu Met Met Tyr Gln Thr Gly Met Lys Ile Leu Asn Gly	
80	185 190 195	
82	agc aat aag aaa agc caa aaa aga gaa gca tat cgg tat ctc caa aag	681
83	Ser Asn Lys Lys Ser Gln Lys Arg Glu Ala Tyr Arg Tyr Leu Gln Lys	
84	200 205 210	
86	gca gca agc atg aac cat acc aaa gcc ctg gag aga gtg tca tat gct	729
87	Ala Ala Ser Met Asn His Thr Lys Ala Leu Glu Arg Val Ser Tyr Ala	
88	215 220 225	
90	ctt tta ttt ggt gat tac ttg cca cag aat atc cag gca gcg aga gag	777
91	Leu Leu Phe Gly Asp Tyr Leu Pro Gln Asn Ile Gln Ala Ala Arg Glu	
92	230 235 240	
94	atg ttt gag aag ctg act gag gaa ggc tct ccc aag gga cag act gct	825
95	Met Phe Glu Lys Leu Thr Glu Glu Gly Ser Pro Lys Gly Gln Thr Ala	
96	245 250 255 260	
98	ctt ggc ttt ctg tat gcc tct gga ctt ggt gtt aat tca agt cag gca	873
99	Leu Gly Phe Leu Tyr Ala Ser Gly Leu Gly Val Asn Ser Ser Gln Ala	
100	265 270 275	
102	aag gct ctt gta tat tat aca ttt gga gct ctt ggg ggc aat cta ata	921
103	Lys Ala Leu Val Tyr Tyr Thr Phe Gly Ala Leu Gly Gly Asn Leu Ile	
104	280 285 290	
106	gcc cac atg gtt ttg ggt tac aga tac tgg gct ggc atc ggc gtc ctc	969
107	Ala His Met Val Leu Gly Tyr Arg Tyr Trp Ala Gly Ile Gly Val Leu	
108	295 300 305	
110	cag agt tgt gaa tct gcc ctg act cac tat cgt ctt gtt gcc aat cat	1017
111	Gln Ser Cys Glu Ser Ala Leu Thr His Tyr Arg Leu Val Ala Asn His	
112	310 315 320	
114	gtt gct agt gat atc tcg cta aca gga ggc tca gta gta cag aga ata	1065
115	Val Ala Ser Asp Ile Ser Leu Thr Gly Gly Ser Val Val Gln Arg Ile	
116	325 330 335 340	
118	cgg ctg cct gat gaa gtg gaa aat cca gga atg aac agt gga atg cta	1113
119	Arg Leu Pro Asp Glu Val Glu Asn Pro Gly Met Asn Ser Gly Met Leu	
120	345 350 355	
122	gaa gaa gat ttg att caa tat tac cag ttc cta gct gaa aaa ggt gat	1161
123	Glu Glu Asp Leu Ile Gln Tyr Tyr Gln Phe Leu Ala Glu Lys Gly Asp	
124	360 365 370	
126	gta caa gca cag gtt ggt ctt gga caa ctg cac ctg cac gga ggg cgt	1209

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130	gga	gta	gaa	cag	aat	cat	cag	aga	gca	ttt	gac	tac	ttc	aat	tta	gca
131	Gly	Val	Glu	Gln	Asn	His	Gln	Arg	Ala	Phe	Asp	Tyr	Phe	Asn	Leu	Ala
132					390				395				400			
134	gca	aat	gct	ggc	aat	tca	cat	gcc	atg	gcc	ttt	ttg	gga	aag	atg	tat
135	Ala	Asn	Ala	Gly	Asn	Ser	His	Ala	Met	Ala	Phe	Leu	Gly	Lys	Met	Tyr
136	405					410					415				420	
138	tcg	gaa	gga	agt	gac	att	gta	cct	cag	agt	aat	gag	aca	gct	ctc	cac
139	Ser	Glu	Gly	Ser	Asp	Ile	Val	Pro	Gln	Ser	Asn	Glu	Thr	Ala	Leu	His
140						425				430				435		
142	tac	ttt	aag	aaa	gct	gct	gac	atg	ggc	aac	cca	gtt	gga	cag	agt	ggg
143	Tyr	Phe	Lys	Lys	Ala	Ala	Asp	Met	Gly	Asn	Pro	Val	Gly	Gln	Ser	Gly
144						440				445				450		
146	ctt	gga	atg	gcc	tac	ctc	tat	ggg	aga	gga	gtt	caa	gtt	aat	tat	gtat
147	Leu	Gly	Met	Ala	Tyr	Leu	Tyr	Gly	Arg	Gly	Val	Gln	Val	Asn	Tyr	Asp
148						455			460				465			
150	cta	gcc	ctt	aag	tat	tcc	cag	aaa	gct	gct	gaa	caa	ggc	tgg	gtg	gtat
151	Leu	Ala	Leu	Lys	Tyr	Phe	Gln	Lys	Ala	Ala	Glu	Gln	Gly	Trp	Val	Asp
152						470			475				480			
154	ggg	cag	cta	cag	ctt	ggt	tcc	atg	tac	tat	aat	ggc	att	gga	gtc	aag
155	Gly	Gln	Leu	Gln	Leu	Gly	Ser	Met	Tyr	Tyr	Asn	Gly	Ile	Gly	Val	Lys
156						485			490				495			500
158	aga	gat	tat	aaa	cag	gcc	ttg	aag	tat	ttt	aat	tta	gct	tct	cag	gga
159	Arg	Asp	Tyr	Lys	Gln	Ala	Leu	Lys	Tyr	Phe	Asn	Leu	Ala	Ser	Gln	Gly
160						505				510				515		
162	ggc	cat	atc	ttg	gct	ttc	tat	aac	cta	gct	cag	atg	cat	gcc	agt	ggc
163	Gly	His	Ile	Leu	Ala	Phe	Tyr	Asn	Leu	Ala	Gln	Met	His	Ala	Ser	Gly
164						520			525				530			
166	acc	ggc	gtg	atg	cga	tca	tgt	cac	act	gca	gtg	gag	ttg	ttt	aag	aat
167	Thr	Gly	Val	Met	Arg	Ser	Cys	His	Thr	Ala	Val	Glu	Leu	Phe	Lys	Asn
168						535			540				545			
170	gta	tgt	gaa	cga	ggc	cgt	tgg	tct	gaa	agg	ctt	atg	act	gcc	tat	aac
171	Val	Cys	Glu	Arg	Gly	Arg	Trp	Ser	Glu	Arg	Leu	Met	Thr	Ala	Tyr	Asn
172						550			555				560			
174	agc	tat	aaa	gat	ggc	gat	tac	aat	gct	gca	gtg	atc	cag	tac	ctc	ctc
175	Ser	Tyr	Lys	Asp	Gly	Asp	Tyr	Asn	Ala	Ala	Val	Ile	Gln	Tyr	Leu	Leu
176						565			570				575			580
178	ctg	gct	gaa	cag	ggc	tat	gaa	gtg	gca	caa	agc	aat	gca	gcc	ttt	att
179	Leu	Ala	Glu	Gln	Gly	Tyr	Glu	Val	Ala	Gln	Ser	Asn	Ala	Ala	Phe	Ile
180						585				590				595		
182	ctt	gat	cag	aga	gaa	gca	agc	att	gta	ggt	gag	aat	gaa	act	tat	ccc
183	Leu	Asp	Gln	Arg	Glu	Ala	Ser	Ile	Val	Gly	Glu	Asn	Glu	Thr	Tyr	Pro
184						600			605				610			
186	aga	gct	ttg	cta	cat	tgg	aac	agg	gcc	gcc	tct	caa	ggc	tat	act	gtg
187	Arg	Ala	Leu	Leu	His	Trp	Asn	Arg	Ala	Ala	Ser	Gln	Gly	Tyr	Thr	Val
188						615			620				625			
190	gct	aga	att	aag	ctc	gga	gac	tac	cat	ttc	tat	ggg	ttt	ggc	acc	gat
191	Ala	Arg	Ile	Lys	Leu	Gly	Asp	Tyr	His	Phe	Tyr	Gly	Phe	Gly	Thr	Asp

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198	caa cac agt gca caa gct atg ttt aat ctg gga tat atg cat gag aaa			2073
199	Gln His Ser Ala Gln Ala Met Phe Asn Leu Gly Tyr Met His Glu Lys			
200	665	670	675	
202	gga ctg ggc att aaa cag gat att cac ctt gcg aaa cgt ttt tat gac			2121
203	Gly Leu Gly Ile Lys Gln Asp Ile His Leu Ala Lys Arg Phe Tyr Asp			
204	680	685	690	
206	atg gca gct gaa gcc agc cca gat gca caa gtt cca gtc ttc cta gcc			2169
207	Met Ala Ala Glu Ala Ser Pro Asp Ala Gln Val Pro Val Phe Leu Ala			
208	695	700	705	
210	ctc tgc aaa ttg ggc gtc gtc tat ttc ttg cag tac ata cgg gaa aca			2217
211	Leu Cys Lys Leu Gly Val Val Tyr Phe Leu Gln Tyr Ile Arg Glu Thr			
212	710	715	720	
214	aac att cga gat atg ttc acc caa ctt gat atg gac cag ctt ttg gga			2265
215	Asn Ile Arg Asp Met Phe Thr Gln Leu Asp Met Asp Gln Leu Leu Gly			
216	725	730	735	740
218	cct gag tgg gac ctt tac ctc atg acc atc att gcg ctg ctg ttg gga			2313
219	Pro Glu Trp Asp Leu Tyr Leu Met Thr Ile Ile Ala Leu Leu Gly			
220	745	750	755	
222	aca gtc ata gct tac agg caa agg cag cac caa gac atg cct gca ccc			2361
223	Thr Val Ile Ala Tyr Arg Gln Arg Gln His Gln Asp Met Pro Ala Pro			
224	760	765	770	
226	agg cct cca ggg cca cg cca gct cca ccc cag cag gag ggg cca cca			2409
227	Arg Pro Pro Gly Pro Arg Pro Ala Pro Pro Gln Gln Glu Gly Pro Pro			
228	775	780	785	
230	gag cag cag cca cca cag taataggcac tgggtccagc cttgatcagt			2457
231	Glu Gln Gln Pro Pro Gln			
232	790			
234	gacagcgaag gaagttatct gctggaaaca cttgcatttg atttaggacc ttggatcagt			2517
236	ggtcacctcc cagaagaggc acggcacaag gaagcattga attcctaaag ctgcttagaa			2577
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252	atatttgtt tttaaaagg gagggttggg aggttctt ttgggtattg tcacacggta			3057
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264	atttatttttta cttgcattt cttttgcac aaagaacaca tcaccttcctt gaattttta			3417
266	aatatgaaat atcattgcca gggatggct tacagtact actattatca atactaaaac			3477
268	tcagagaatc aaagatggat taaactcagt ggttgcata agccaaaacc tgttgtact			3537

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276 taattacaca cgtgaaataa ttacagctt aactgaattt gtatttcattt ttattgtcag 3777
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280 ctatgcctac tgatgtcagt atgttatac taaccctcat gctttttcc cagaatccct 3897
282 catctgccag aaaactgaa aagtttattt cttagagttt tgtactgctt tgattttga 3957
284 agttgggtta gtatgttagaa ctagatttaa ctagtctata atgaacatga aggctttat 4017
286 atatgaagtt gtatacctt ttgtgttttag agaattatgg gaaacctgtt aagcaaaact 4077
288 ttcccccag ataattgtttt ccaaattcga agagttagtc accaagagag ccatatgtat 4137
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/25/2006
PATENT APPLICATION: US/10/592,918 TIME: 10:34:46

Input Set : A:\L7350.0011 SEQUENCE LISTING.txt
Output Set: N:\CRF4\09252006\J592918.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5,6,7,8,9,10,11,12,13,14,15

VERIFICATION SUMMARY DATE: 09/25/2006
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Input Set : A:\L7350.0011 SEQUENCE LISTING.txt
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date